SEQUENCE LISTING

```
<110>  Callen, Walter
       Richardson, Toby
       Frey, Gerhard
       Miller, Carl
       Kazaoka, Martin
       Short, Jay
       Mathur, Eric

<120>  ENZYMES HAVING ALPHA AMYLASE ACTIVITY
       AND METHODS OF USE THEREOF

<130>  09010-107001

<140>  10/081,739
<141>  2002-02-21

<150>  60/270,495
<151>  2001-02-21

<150>  60/270,496
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<150>  60/291,122
<151>  2001-05-14

<160>  69

<170>  FastSEQ for Windows Version 4.0

<210>  1
<211>  1311
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetically generated

<400>  1
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gtgccttcag gaggaatatg gtgggacaca atacggcaga agataccgga gtggtacgat     120
gccggaatct ccgcaatatg gattcccccg gcgagcaagg gcatgggcgg cgcctattcg     180
atgggctacg acccctacga cttctttgac ctcggtgagt acgaccagaa gggaacggta     240
gagacgcgct ttggctccaa gcaggagctc gtgaacatga taaacaccgc ccacgcctat     300
ggcatgaagg taatagccga tatagtcatc aaccaccgcg ccggcggtga cctggagtgg     360
aacccccttcg tgaacgacta tacctggacc gacttctcaa aggtcgcgtc gggtaaatac     420
acggccaact acctcgactt ccacccgaac gagctccatg cgggcgattc cggaacattt     480
ggaggctatc ccgacatatg ccacgacaag agctgggacc agtactggct ctgggccagc     540
caggagagct acgcggcata tctcaggagc atcggcatcg atgcctggcg cttcgactac     600
gtcaagggct atgctccctg ggtcgtcaag gactggctga actggtgggg aggctgggcg     660
gttggagagt actgggacac caacgtcgac gctgttctca actgggcata ctcgagcggt     720
gccaaggtct ttgacttcgc cctctactac aagatggatg aggcctttga caacaaaaac     780
attccagcgc tcgtctctgc ccttcagaac ggccagactg ttgtctcccg cgacccgttc     840
aaggccgtaa cctttgtagc aaaccacgac accgatataa tctggaacaa gtatccagcc     900
tacgcgttca tcctcaccta cgagggccag ccgacaatat tctaccgcga ctacgaggag     960
```

```
tggctcaaca aggataagct caagaacctc atctggatac atgagaacct cgccggagga   1020
agcaccgaca tagtctacta cgataacgat gaactcatct tcgtcaggaa cggctacggg   1080
gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt   1140
tatgtgccga agttcgcggg cgcgtgcatc cacgagtata ctggtaacct cggaggctgg   1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgaccct   1260
gccaacgggc agtatggcta ctccgtgtgg agctactgcg gggtgggctg a           1311
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<210> 2
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically engineered

<400> 2

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Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg
                20                  25                  30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
            35                  40                  45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
        50                  55                  60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65                  70                  75                  80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
                85                  90                  95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
                100                 105                 110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
            115                 120                 125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
        130                 135                 140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145                 150                 155                 160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
                165                 170                 175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
                180                 185                 190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
            195                 200                 205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
        210                 215                 220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225                 230                 235                 240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
                245                 250                 255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
                260                 265                 270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
            275                 280                 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
        290                 295                 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305                 310                 315                 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn
```

```
                325                330                335
Leu Ala Gly Gly Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu
                340                345                350
Ile Phe Val Arg Asn Gly Tyr Gly Asp Lys Pro Gly Leu Ile Thr Tyr
                355                360                365
Ile Asn Leu Gly Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys
            370                375                380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
        385                390                395                400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
                405                410                415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
                420                425                430
Cys Gly Val Gly
                435
```

<210> 3
<211> 1419
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 3
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atgttcctgc tcgcgttttt gctcactgcc tcgctgttct gcccaacagg acagcccgcc     60
aaggctgccg caccgtttaa cggcaccatg atgcagtatt ttgaatggta cttgccggat    120
gatggcacgt tatggaccaa agtggccaat gaagccaaca acttatccag ccttggcatc    180
accgctcttt ggctgccgcc cgcttacaaa ggaacaagcc gcagcgacgt agggtacgga    240
gtatacgact tgtatgacct cggcgaattc aatcaaaaag ggaccgtccg cacaaaatac    300
ggaacaaaag ctcaatatct tcaagccatt caagccgccc acgccgctgg aatgcaagtg    360
tacgccgatg tcgtgttcga ccataaaggc ggcgctgacg gcacggaatg ggtggacgcc    420
gtcgaagtca atccgtccga ccgcaaccaa gaaatctcgg gcacctatca aatccaagca    480
tggacgaaat ttgattttcc cgggcggggc aacacctact ccagctttaa gtggcgctgg    540
taccattttg acggcgttga ttgggacgaa agccgaaaat tgagccgcat ttacaaattc    600
cgcggcatcg gcaaagcgtg ggattgggaa gtagacacgg aaaacggaaa ctatgactac    660
ttaatgtatg ccgaccttga tatggatcat cccgaagtcg tgaccgagct gaaaaactgg    720
gggaaatggt atgtcaacac aacgaacatt gatgggttcc ggcttgatgc cgtcaagcat    780
attaagttca gttttttcc tgattggttg tcgtatgtgc gttctcagac tggcaagccg    840
ctatttaccg tcggggaata ttggagctat gacatcaaca agttgcacaa ttacattacg    900
aaaacagacg gaacgatgtc tttgtttgat gccccgttac acaacaaatt ttataccgct    960
tccaaatcag ggggcgcatt tgatatgcgc acgttaatga ccaatactct catgaaagat   1020
caaccgacat tggccgtcac cttcgttgat aatcatgaca ccgaacccgg ccaagcgctg   1080
cagtcatggg tcgacccatg gttcaaaccg ttggcttacg cctttattct aactcggcag   1140
gaaggatacc cgtgcgtctt ttatggtgac tattatggca ttccacaata taacattcct   1200
tcgctgaaaa gcaaaatcga tccgctcctc atcgcgcgca gggattatgc ttacggaacg   1260
caacatgatt atcttgatca ctccgacatc atcgggtgga caagggaagg ggtcactgaa   1320
aaaccaggat ccgggctggc cgcactgatc accgatgggc cgggaggaag caaatggatg   1380
tactgttggc aaacaacacg ctggaaaagt gttctatga                          1419
```

<210> 4
<211> 1539
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 4

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atgaaacaac aaaaacggct ttacgcccga ttgctgacgc tgttatttgc gctcatcttc        60
ttgctgcctc attctgcagc agcggcggca aatcttaatg ggacgctgat gcagtatttt       120
gaatggtaca tgcccaatga cggccaacat tggaagcgct tgcaaaacga ctcggcatat       180
ttggctgaac acggtattac tgccgtctgg attcccccgg catataaggg aacgagccaa       240
gcggatgtgg gctacggtgc ttacgacctt tatgatttag gggagtttca tcaaaaaggg       300
acggttcgga caaagtacgg cacaaaagga gagctgcaat ctgcgatcaa aagtcttcat       360
tcccgcgaca ttaacgttta cggggatgtg gtcatcaacc acaaaggcgg cgctgatgcg       420
accgaagatg taaccgcggt tgaagtcgat cccgctgacc gcaaccgcgt aatttcagga       480
gaacaccgaa ttaaagcctg gacacatttt cattttccgg ggcgcggcag cacatacagc       540
gattttaaat ggcattggta ccattttgac ggaaccgatt gggacgagtc ccgaaagctg       600
aaccgcatct ataagtttca aggaaaggct tgggattggg aagtttccaa tgaaaacggc       660
aactatgatt atttgatgta tgccgacatc gattatgacc atcctgatgt cgcagcagaa       720
attaagagat ggggcacttg gtatgccaat gaactgcaat tggacggttt ccgtcttgat       780
gctgtcaaac acattaaatt ttctttttg cgggattggg ttaatcatgt cagggaaaaa       840
acggggaagg aaatgtttac ggtagctgaa tattggcaga atgacttggg cgcgctggaa       900
aactatttga acaaaacaaa ttttaatcat tcagtgtttg acgtgccgct tcattatcag       960
ttccatgctg catcgacaca gggaggcggc tatgatatga ggaaattgct gaacggtacg      1020
gtcgtttcca agcatccgtt gaaagcggtt acatttgtcg ataaccatga tacacagccg      1080
gggcaatcgc ttgagtcgac tgtccaaaca tggtttaagc cgcttgctta cgctttcatt      1140
ctcacaaggg aatctggata ccctcaggtt ttctacgggg atatgtacgg gacgaaagga      1200
gactcccagc gcgaaattcc tgccttgaaa cacaaaattg aaccgatctt aaaagcgaga      1260
aaacagtatg cgtacggagc acagcatgat tatttcgacc accatgacat tgtcggctgg      1320
acaagggaag gcgacagctc ggttgcaaat tcaggtttgg cggcattaat aacagacgga      1380
cccggtgggg caaagcgaat gtatgtcggc cggcaaaacg ccggtgagac atggcatgac      1440
attaccggaa accgttcgga gccggttgtc atcaattcgg aaggctgggg agagtttcac      1500
gtaaacggcg ggtcggtttc aatttatgtt caaagatag                             1539
```

<210> 5
<211> 1395
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 5

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gtggtgcaca tgaagttgaa gtaccttgcc ttagttttgt tggctgtggc ttcgataggc        60
ctactctcga ctccagtggg tgctgccaag tactccgaac tcgaagaggg cggtgttata       120
atgcaggcct tctactggga tgttcccgga ggggaatct ggtgggacac cataagacag       180
aaaatcccgg agtggtacga cgctggaatc tcggcgatat ggattcctcc agctagcaaa       240
gggatgggcg gtggttattc catgggctac gatccctacg atttctttga cctcggcgag       300
tactatcaga agggaacagt tgagacgcgc ttcggctcaa aggaggaact ggtgaacatg       360
ataaacaccg cacactccta tggcataaag gtgatagcgg acatagtcat aaaccaccgc       420
gccggtggag accttgagtg gaacccctt gtaaacaact atacttggac agacttctcc       480
aaggtcgcct ccggtaaata cacggccaac taccttgact tccacccaaa cgaggtcaag       540
tgctgcgatg agggtacatt tggtgacttt ccggacatcg cccacgagaa gagctgggat       600
cagtactggc tctgggcaag caatgagagc tacgccgcat atctccggag cataggggatc       660
gatgcatggc gtttcgacta cgtcaaaggt tacggagcgt gggttgttaa tgactggctc       720
agctggtggg gaggctgggc cgttggagag tactgggaca cgaacgttga tgcactcctt       780
aactgggcat acgacagcgg tgccaaggtc tttgacttcc cgctctacta caagatggac       840
gaagcctttg acaacaccaa catccccgct ttggtttacg ccctccagaa cggaggaaca       900
gtcgtttccc gcgatccctt caaggcagta actttcgttg ccaaccacga tacagatata       960
atctggaaca gtatccggc ttatgcgttc atccttacct atgagggaca gcctgttata      1020
ttttaccgcq actacgaggq qtqqctcaac aaqqataaqc ttaacaacct tatctqqata      1080
cacgagcacc ttgccggagg aagtaccaag atcctctact acgataacga tgagctaata      1140
```

```
ttcatgaggg agggctacgg gagcaagccg ggcctcataa cctacataaa cctcggaaac    1200
gactgggccg agcgctgggt gaacgtcggc tcaaagtttg ccggctacac aatccatgaa    1260
tacacaggca atctcggtgg ctgggttgac aggtgggttc agtacgatgg atgggttaaa    1320
ctgacggcac ctcctcatga tccagccaac ggatattacg gctactcagt ctggagctac    1380
gcaggcgtcg gatga                                                     1395
```

<210> 6
<211> 1386
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 6
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atgaagaagt ttgtcgccct gttcataacc atgttttttcg tagtgagcat ggcagtcgtt      60
gcacagccag ctagcgccgc aaagtattcc gagctcgaag aaggcggcgt tataatgcag     120
gccttctact gggacgtccc aggtggagga atctggtggg acaccatcag gagcaagata     180
ccggagtggt acgaggcggg aatatccgcc atttggattc cgccagccag caaggggatg     240
agcggcggtt actcgatggg ctacgatccc tacgatttct ttgacctcgg cgagtacaac     300
cagaagggaa ccatcgaaac gcgctttggc tctaaacagg agctcatcaa tatgataaac     360
acggcccatg cctacggcat aaaggtcata gcggacatcg tcataaacca ccgcgcaggc     420
ggagacctcg agtggaaccc gttcgttggg gactacacct ggacggactt ctcaaaggtg     480
gcctcgggca aatatactgc caactacctc gacttccacc ccaacgaggt caagtgctgt     540
gacgagggca catttggagg cttcccagac atagcccacg agaagagctg ggaccagcac     600
tggctctggg cgagcgatga gagctacgcc gcctacctaa ggagcatcgg cgttgatgcc     660
tggcgctttg actacgtgaa gggctacgga gcgtgggtcg tcaaggactg gctcaactgg     720
tggggcggct gggccgttgg cgagtactgg gacaccaacg ttgatgcact cctcaactgg     780
gcctactcga gcggcgccaa ggtcttcgac ttcccgctct actacaagat ggatgaggcc     840
tttgacaaca aaaacattcc agcgctcgtc tctgcccttc agaacggcca gactgttgtc     900
tcccgcgacc cgttcaaggc cgtaaccttt gtagcaaacc acgacaccga tataatctgg     960
aacaagtacc ttgcttatgc tttcatcctc acctacgaag gccagcccgt catattctac    1020
cgcgactacg aggagtggct caacaaggac aggttgaaca acctcatatg gatacacgac    1080
cacctcgcag gtggaagcac gagcatagtc tactacgaca gcgacgagat gatcttcgtg    1140
aggaacggct atggaagcaa gcctggcctt ataacttaca tcaacctcgg ctcgagcaag    1200
gttggaaggt gggtttatgt gccgaagttc gcgggcgcgt gcatccacga gtatactggt    1260
aacctcggag gctgggtaga caagtacgtc tactcaagcg gctgggtcta tctcgaagct    1320
ccagcttacg accctgccaa cgggcagtat ggctactccg tgtggagcta ttgcggtgtt    1380
gggtga                                                             1386
```

<210> 7
<211> 472
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 7
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Met Phe Leu Leu Ala Phe Leu Leu Thr Ala Ser Leu Phe Cys Pro Thr
  1               5                  10                  15
Gly Gln Pro Ala Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln
             20                  25                  30
Tyr Phe Glu Trp Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val
         35                  40                  45
Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp
     50                  55                  60
```

Leu Pro Pro Ala Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly
65   70   75   80
Val Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val
                85   90   95
Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala
            100   105   110
Ala His Ala Ala Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His
        115   120   125
Lys Gly Gly Ala Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn
        130   135   140
Pro Ser Asp Arg Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala
145   150   155   160
Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe
            165   170   175
Lys Trp Arg Trp Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg
            180   185   190
Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp
            195   200   205
Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala
210   215   220
Asp Leu Asp Met Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp
225   230   235   240
Gly Lys Trp Tyr Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp
            245   250   255
Ala Val Lys His Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr
            260   265   270
Val Arg Ser Gln Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp
            275   280   285
Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly
    290   295   300
Thr Met Ser Leu Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala
305   310   315   320
Ser Lys Ser Gly Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr
            325   330   335
Leu Met Lys Asp Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His
            340   345   350
Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe
    355   360   365
Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro
    370   375   380
Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro
385   390   395   400
Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr
            405   410   415
Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly
            420   425   430
Trp Thr Arg Glu Gly Val Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala
            435   440   445
Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys Trp Met Tyr Cys Trp Gln
    450   455   460
Thr Thr Arg Trp Lys Ser Val Leu
465   470

<210> 8
<211> 512
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 8

```
Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
1               5                   10                  15
Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Asn Leu
            20                  25                  30
Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro Asn Asp Gly
        35                  40                  45
Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu Ala Glu His
    50                  55                  60
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
65                  70                  75                  80
Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
                85                  90                  95
His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
            100                 105                 110
Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
        115                 120                 125
Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
    130                 135                 140
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
145                 150                 155                 160
Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
                165                 170                 175
Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr
            180                 185                 190
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly
            195                 200                 205
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr
    210                 215                 220
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu
225                 230                 235                 240
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly
                245                 250                 255
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp
            260                 265                 270
Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val
    275                 280                 285
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn
    290                 295                 300
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln
305                 310                 315                 320
Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu
                325                 330                 335
Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr Phe
            340                 345                 350
Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val
            355                 360                 365
Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu
    370                 375                 380
Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly
385                 390                 395                 400
Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile
                405                 410                 415
```

```
Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
            420             425             430
Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
            435             440             445
Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
    450             455             460
Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
465             470             475             480
Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp
            485             490             495
Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg
            500             505             510
```

<210> 9
<211> 464
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 9
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Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val
1               5               10              15
Ala Ser Ile Gly Leu Leu Ser Thr Pro Val Gly Ala Ala Lys Tyr Ser
            20              25              30
Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val
            35              40              45
Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu
    50              55              60
Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys
65              70              75              80
Gly Met Gly Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe
            85              90              95
Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly
            100             105             110
Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr Gly
            115             120             125
Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp
    130             135             140
Leu Glu Trp Asn Pro Phe Val Asn Asn Tyr Thr Trp Thr Asp Phe Ser
145             150             155             160
Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro
            165             170             175
Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Asp Phe Pro Asp
            180             185             190
Ile Ala His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn
    195             200             205
Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg
    210             215             220
Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp Leu
225             230             235             240
Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val
            245             250             255
Asp Ala Leu Leu Asn Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp
            260             265             270
Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile
```

```
                275                      280                      285
Pro Ala Leu Val Tyr Ala Leu Gln Asn Gly Gly Thr Val Val Ser Arg
    290                      295                      300
Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile
305                      310                      315                      320
Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly
                325                      330                      335
Gln Pro Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp
                340                      345                      350
Lys Leu Asn Asn Leu Ile Trp Ile His Glu His Leu Ala Gly Gly Ser
                355                      360                      365
Thr Lys Ile Leu Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Met Arg Glu
    370                      375                      380
Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Asn
385                      390                      395                      400
Asp Trp Ala Glu Arg Trp Val Asn Val Gly Ser Lys Phe Ala Gly Tyr
                405                      410                      415
Thr Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Arg Trp
                420                      425                      430
Val Gln Tyr Asp Gly Trp Val Lys Leu Thr Ala Pro Pro His Asp Pro
                435                      440                      445
Ala Asn Gly Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Ala Gly Val Gly
    450                      455                      460
```

```
<210> 10
<211> 461
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 10
Met Lys Lys Phe Val Ala Leu Phe Ile Thr Met Phe Phe Val Val Ser
  1               5                    10                      15
Met Ala Val Val Ala Gln Pro Ala Ser Ala Ala Lys Tyr Ser Glu Leu
                20                      25                      30
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Gly
                35                      40                      45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Ser Lys Ile Pro Glu Trp Tyr
    50                      55                      60
Glu Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
65                      70                      75                      80
Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
                85                      90                      95
Gly Glu Tyr Asn Gln Lys Gly Thr Ile Glu Thr Arg Phe Gly Ser Lys
                100                     105                     110
Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
                115                     120                     125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
    130                     135                     140
Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
145                     150                     155                     160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
                165                     170                     175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
                180                     185                     190
```

His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
      195   200   205

Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
   210   215   220

Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
225   230   235   240

Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
          245   250   255

Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
          260   265   270

Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala
          275   280   285

Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro
          290   295   300

Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
305   310   315   320

Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
          325   330   335

Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
          340   345   350

Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
          355   360   365

Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr
   370   375   380

Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
385   390   395   400

Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
          405   410   415

Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser
          420   425   430

Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly
          435   440   445

Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
   450   455   460

<210> 11
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gaacactagt aggaggtaac ttatggcaaa gtattccgag ctcgaag   47

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
gaacggtctc attccgccag ccagcaaggg gatgagcgg   39

```
<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gaaccgtctc aaaacacggc ccatgcctac ggc                          33


<210> 14
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
gaacgtctca cctcgacttc caccccaacg aggtcaag                     38


<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacgtctca ggcgctttga ctacgtgaag ggc                          33


<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gaacggtctc aacaagatgg atgaggcctt tg                           32


<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gaaccgtctc acgatataat ctggaacaag taccttgc                     38


<210> 18
<211> 35
```

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gaaccgtctc agaagcacga gcatagttta ctacg   35

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
gaaccgtctc aaaggtgggt ttatgtgccg   30

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
gaacgtctca ggaatccaaa tggcggatat tcccgc   36

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gaacggtctc agtttatcat attgatgagc tcc   33

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gaaccgtctc agaggtagtt ggcagtatat ttg   33

<210> 23
<211> 31
<212> DNA
<213> Artificial Sequence

```
<220>
<223> Primer

<400> 23
gaacgtctca cgccaggcat caacgccgat g                              31

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gaacgtctca ttgtagtaga gcgggaagtc                               30

<210> 25
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
gaacggtctc aatcggtgtc gtggtttgct ac                            32

<210> 26
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
gaaccgtctc acttccacct gcgaggtggt c                             31

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
gaaccgtctc accttccaac cttgctcgag c                             31

<210> 28
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
```

<223> Primer

<400> 28
tcgagactga ctctcaccca acaccgcaat agc   33

<210> 29
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 29
gaacactagt aggaggtaac ttatggccaa gtacctggag ctcgaagagg   50

<210> 30
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
gaacggtctc attcccccgg cgagcaaggg c   31

<210> 31
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
gaaccgtctc aaaacaccgc ccacgcctac gg   32

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
gaacgtctca cctcgacttc caccccaac   29

<210> 33
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 33
gaacgtctca ggcgcttcga ctacgtcaag g   31

<210> 34
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34
gaacggtctc aacaagatgg acgcggcctt tgac   34

<210> 35
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 35
gaaccgtctc acgatataat ttggaacaag taccc   35

<210> 36
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 36
gaaccgtctc agaagcaccg acatagtcta c   31

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 37
gaaccgtctc aaaggtgggt ctacgttccg   30

<210> 38
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 38
gaacgtctca ggaatccata ttgcggagat tccggc   36

```
<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 39
gaacggtctc agtttatcat gttcacgagc tc                              32

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 40
gaaccgtctc agaggtagtt ggccgtgtac ttg                             33

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 41
gaacgtctca gccatgcgtc aacgccgatg                                 30

<210> 42
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
gaacgtctca ttgtagtaga gcgggaagtc g                               31

<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
gaacggtctc aatcggtgtc gtggtttgca acg                             33

<210> 44
```

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 44
gaaccgtctc acttccaccg gcgaggtggt cgtg   34

<210> 45
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
gaaccgtctc accttccggc cttgctcgag cc   32

<210> 46
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 46
tcgagactga ctctcagccc accccgcagt agctc   35

<210> 47
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 47
gaacactagt aggaggtaac ttatggccaa gtactccgag ctggaagagg   50

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 48
gaacggtctc attcctcccg cgagcaaggg   30

<210> 49
<211> 31
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 49
gaaccgtctc aaaacaccgc ccacgcctat g   31

<210> 50
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 50
gaacgtctca cctcgacttc cacccgaacg agc   33

<210> 51
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 51
gaacgtctca ggcgcttcga ctacgtcaag g   31

<210> 52
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 52
gaacggtctc aacaagatgg acgaggcctt cg   32

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
gaaccgtctc acgatataat ctggaacaag   30

<210> 54
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 54
gaaccgtctc agaagcactg acatcgttta ctacg   35

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 55
gaaccgtctc aaaggtgggt ttacgttccg   30

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 56
gaacgtctca ggaatccata tcgccgaaat   30

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 57
gaacggtctc agtttatcat gtttatgagc   30

<210> 58
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 58
gaaccgtctc agaggtagtt ggccgtgtat ttac   34

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

```
<400> 59
gaacgtctca cgccaggcat cgatgccgat                                    30


<210> 60
<211> 34
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer


<400> 60
gaacgtctca ttgtagtaga gggcgaagtc aaag                               34


<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer


<400> 61
gaacggtctc aatcggtatc gtggttggct acaaac                             36


<210> 62
<211> 34
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer


<400> 62
gaaccgtctc acttcctccg gcgaggttgt catg                               34


<210> 63
<211> 32
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer


<400> 63
gaaccgtctc accttccggc tttgcttgag gc                                 32


<210> 64
<211> 36
<212> DNA
<213> Artificial Sequence


<220>
<223> Primer


<400> 64
```

```
tcgagactga ctctcaccca acaccgcagt agctcc                          36
```

```
<210> 65
<211> 38
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Primer
```

```
<400> 65
cacacagcag caaccaacct cgagactgac tctcascc                        38
```

```
<210> 66
<211> 1299
<212> DNA
<213> Unknown
```

```
<220>
<223> Obtained from an environmental sample
```

```
<400> 66
atggctctgg aagagggcgg gctcataatg caggccttct actgggacgt ccccatggga    60
ggaatctggt gggacacgat agcccagaag atacccgact gggcaagcgc cgggatttcg   120
gcgatatgga tccctcccgc gagcaagggt atgagcggcg gctattcgat gggctacgac   180
ccctacgatt attttgacct cggtgagtac taccagaagg gaacggtgga aacgaggttc   240
ggctcaaagc aggagctcat aaacatgata aacaccgccc acgcctatgg catgaaggta   300
atagccgata tagtcatcaa ccaccgcgcc ggcggtgacc tggagtggaa ccccttcgtg   360
aacgactata cctggaccga cttctcaaag gtcgcgtcgg gtaaatacac ggccaactac   420
ctcgacttcc acccgaacga gctccatgcg ggcgattccg gaacatttgg aggctatccc   480
gacatatgcc acgacaagag ctgggaccag tactggctct gggccagcca ggagagctac   540
gcggcatatc tcaggagcat cggcatcgat gcctggcgct cgactacgt caagggctat    600
gctccctggg tcgtcaagga ctggctgaac tggtggggag gctgggcggt tggagagtac   660
tgggacacca acgtcgacgc tgttctcaac tgggcatact cgagcggtgc caaggtcttt   720
gacttcgccc tctactacaa gatggacgag gccttcgata caacaacat tcccgccctg    780
gtggacgccc tcagatacgg tcagacagtg gtcagccgcg acccgttcaa ggctgtgacg   840
tttgtagcca accacgatac cgacataatc tggaacaagt atccagccta cgcgttcatc   900
ctcacctacg agggccagcc gacaatattc taccgcgact acgaggagtg gctcaacaag   960
gataagctca agaacctcat ctggatacat gacaacctcg ccggagggag cactgacatc  1020
gtttactacg acaacgacga gctgatattc gtgagaaacg gctacggaag caagccggga  1080
ctgataacat acatcaacct cgcctcaagc aaagccggaa ggtgggttta cgttccgaag  1140
ttcgcaggct cgtgcataca cgagtacacc ggcaatctcg gcggctgggt ggacaagtgg  1200
gtggactcaa gcggctgggt ctacctcgag gctcctgccc acgacccggc caacggccag  1260
tacggctact ccgtctggag ctactgcggt gttgggtga                         1299
```

```
<210> 67
<211> 432
<212> PRT
<213> Unknown
```

```
<220>
<223> Obtained from an environmental sample
```

```
<400> 67
Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
 1               5                  10                  15
Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro
```

```
                20                      25                      30
Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser
        35                      40                      45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr
        50                      55                      60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe
65                      70                      75                      80
Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr
                85                      90                      95
Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly
                100                     105                     110
Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe
        115                     120                     125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His
        130                     135                     140
Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly Gly Tyr Pro
145                     150                     155                     160
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser
                165                     170                     175
Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp
                180                     185                     190
Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val Val Lys Asp Trp
        195                     200                     205
Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn
        210                     215                     220
Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe
225                     230                     235                     240
Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn
                245                     250                     255
Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln Thr Val Val Ser
                260                     265                     270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp
        275                     280                     285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu
        290                     295                     300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys
305                     310                     315                     320
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu Ala Gly Gly
                325                     330                     335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg
                340                     345                     350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Ala
                355                     360                     365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser
        370                     375                     380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp
385                     390                     395                     400
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro
                405                     410                     415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
                420                     425                     430
```

<220>
<223> Obtained from an environmental sample

<400> 68
```
atgaagcctg cgaaactcct cgtctttgtg ctcgtagtct ctatcctcgc ggggctctac          60
gcccagcccg cggggggcggc caagtacctg gagctcgaag agggcggcgt cataatgcag        120
gcgttctact gggacgtgcc ttcaggagga atatggtggg acacaatacg gcagaagata        180
ccggagtggt acgatgccgg aatctccgca atatggattc ccccggcgag caagggcatg        240
ggcggcgcct attcgatggg ctacgacccc tacgacttct ttgacctcgg tgagtacgac        300
cagaagggaa cggtagagac gcgctttggc tccaagcagg agctcgtgaa catgataaac        360
accgcccacg cctacggcat caaggtcatc gcagacatag taatcaacca ccgcgccgga        420
ggagaccttg agtggaaccc cttcgtcaat gactacacct ggacggactt ctcgaaggtc        480
gcttccggca agtacacggc caactacctc gacttccacc ccaacgaggt caagtgctgc        540
gacgagggca ccttggagg gttcccggac atagcccacg agaagagctg ggaccagtac        600
tggctctggg cgagcaacga gagctacgcc gcctacctca ggagcatcgg cgttgacgca        660
tggcgcttcg actacgtcaa gggctacgga gcgtgggtcg tcaaggactg gctggactgg        720
tggggaggct gggccgtcgg ggagtactgg gacacaaacg ttgatgcact gctcaactgg        780
gcctactcga gcgatgcaaa agtcttcgac ttcccgctct actacaagat ggacgcggcc        840
tttgacaaca agaacattcc cgcactcgtc gaggccctca gaacggggg cacagtcgtc        900
agccgcgacc cgtttaaggc cgtaaccttc gttgcaaacc acgacacgga cataatttgg        960
aacaagtacc cggcctacgc cttcatcctc acctacgagg gccagccgac gatattctac       1020
cgcgactacg aggagtggct caacaaggac aggctcaaga acctcatctg gatacacgac       1080
cacctcgccg gtggaagcac cgacatagtc tactacgata acgatgaact catcttcgtc       1140
aggaacggct acggggacaa gccgggggctt ataacctaca tcaacctagg ctcgagcaag      1200
gccgggaggt gggtctacgt tccgaagttc gcgggagcgt gcatccacga gtacaccggc       1260
aacctcggcg gctgggtgga caagtgggtg gactcaagcg ggtgggtgta cctcgaggcc       1320
cctgcccacg acccggccaa cggctattac ggctactccg tctggagcta ctgcggggtg       1380
ggctga                                                                    1386
```

<210> 69
<211> 461
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 69
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Met Lys Pro Ala Lys Leu Leu Val Phe Val Leu Val Val Ser Ile Leu
 1               5                  10                  15
Ala Gly Leu Tyr Ala Gln Pro Ala Gly Ala Ala Lys Tyr Leu Glu Leu
            20                  25                  30
Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val Pro Ser
        35                  40                  45
Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu Trp Tyr
    50                  55                  60
Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys Gly Met
65                  70                  75                  80
Gly Gly Ala Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe Asp Leu
                85                  90                  95
Gly Glu Tyr Asp Gln Lys Gly Thr Val Glu Thr Arg Phe Gly Ser Lys
            100                 105                 110
Gln Glu Leu Val Asn Met Ile Asn Thr Ala His Ala Tyr Gly Ile Lys
        115                 120                 125
Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp Leu Glu
    130                 135                 140
Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe Ser Lys Val
```

```
145               150                    155              160
Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro Asn Glu
                165                    170              175
Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala
                180                    185              190
His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn Glu Ser
                195                    200              205
Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
    210                    215              220
Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asp Trp
225                    230              235              240
Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
                245              250              255
Leu Leu Asn Trp Ala Tyr Ser Ser Asp Ala Lys Val Phe Asp Phe Pro
                260              265              270
Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp Asn Lys Asn Ile Pro Ala
                275              280              285
Leu Val Glu Ala Leu Lys Asn Gly Gly Thr Val Val Ser Arg Asp Pro
    290              295              300
Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
305              310              315                    320
Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
                325              330                    335
Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
                340              345              350
Lys Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Asp
                355              360              365
Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg Asn Gly Tyr
    370              375              380
Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
385              390              395              400
Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
                405              410              415
Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp Val Asp Ser
                420              425              430
Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro Ala Asn Gly
                435              440              445
Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
    450              455              460
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